SEQUENCE LISTING

<110> HANSSON, HANS-ARNE
JENNISCHE, EVA
LANGE, STEFAN
LON-NROTH, IVAR
ERIKSSON, PETER
PERSSON, ANDERS

<120> NOVEL USE OF ANTISECRETORY FACTOR

<130> 1003301-000258

<140>
<141>

<150> PCT/SE04/001369
<151> 2004-09-24

<150> GB 0322645.3
<151> 2003-09-26

<160> 6

<170> PatentIn Ver. 3.3

<210> 1
<211> 382
<212> PRT
<213> Homo sapiens

<400> 1

```
Met Val Leu Glu Ser Thr Met Val Cys Val Asp Asn Ser Glu Tyr Met
  1               5                  10                  15

Arg Asn Gly Asp Phe Leu Pro Thr Arg Leu Gln Ala Gln Gln Asp Ala
             20                  25                  30

Val Asn Ile Val Cys His Ser Lys Thr Arg Ser Asn Pro Glu Asn Asn
         35                  40                  45

Val Gly Leu Ile Thr Leu Ala Asn Asp Cys Glu Val Leu Thr Thr Leu
     50                  55                  60

Thr Pro Asp Thr Gly Arg Ile Leu Ser Lys Leu His Thr Val Gln Pro
 65                  70                  75                  80

Lys Gly Lys Ile Thr Phe Cys Thr Gly Ile Arg Val Ala His Leu Ala
                 85                  90                  95

Leu Lys His Arg Gln Gly Lys Asn His Lys Met Arg Ile Ile Ala Phe
            100                 105                 110

Val Gly Ser Pro Val Glu Asp Asn Glu Lys Asp Leu Val Lys Leu Ala
        115                 120                 125

Lys Arg Leu Lys Lys Glu Lys Val Asn Val Asp Ile Ile Asn Phe Gly
    130                 135                 140
```

```
Glu Glu Glu Val Asn Thr Glu Lys Leu Thr Ala Phe Val Asn Thr Leu
145                 150                 155                 160

Asn Gly Lys Asp Gly Thr Gly Ser His Leu Val Thr Val Pro Pro Gly
                165                 170                 175

Pro Ser Leu Ala Asp Ala Leu Ile Ser Ser Pro Ile Leu Ala Gly Glu
            180                 185                 190

Gly Gly Ala Met Leu Gly Leu Gly Ala Ser Asp Phe Glu Phe Gly Val
        195                 200                 205

Asp Pro Ser Ala Asp Pro Glu Leu Ala Leu Ala Leu Arg Val Ser Met
    210                 215                 220

Glu Glu Gln Arg His Ala Gly Gly Gly Ala Arg Arg Ala Ala Arg Ala
225                 230                 235                 240

Ser Ala Ala Glu Ala Gly Ile Ala Thr Thr Gly Thr Glu Asp Ser Asp
                245                 250                 255

Asp Ala Leu Leu Lys Met Thr Ile Ser Gln Gln Glu Phe Gly Arg Thr
            260                 265                 270

Gly Leu Pro Asp Leu Ser Ser Ser Thr Glu Glu Glu Glu Ile Ala Tyr
        275                 280                 285

Ala Met Gln Met Ser Leu Gln Gly Ala Glu Phe Gly Gln Ala Glu Ser
    290                 295                 300

Ala Asp Ile Asp Ala Ser Ser Ala Met Asp Thr Ser Glu Pro Ala Lys
305                 310                 315                 320

Glu Glu Asp Asp Tyr Asp Val Met Gln Asp Pro Glu Phe Leu Gln Ser
                325                 330                 335

Val Leu Glu Asn Leu Pro Gly Val Asp Pro Asn Asn Glu Ala Ile Arg
            340                 345                 350

Asn Ala Met Gly Ser Leu Pro Pro Arg Pro Pro Arg Thr Ala Arg Arg
        355                 360                 365

Thr Arg Arg Arg Lys Thr Arg Ser Glu Thr Gly Gly Lys Gly
    370                 375                 380
```

<210> 2
<211> 1323
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (63)..(1208)

<400> 2
aattggagga gttgttgtta ggccgtcccg gagacccggt cgggagggag gaaggtggca 60

```
ag atg gtg ttg gaa agc act atg gtg tgt gtg gac aac agt gag tat    107
   Met Val Leu Glu Ser Thr Met Val Cys Val Asp Asn Ser Glu Tyr
     1               5                  10                  15

atg cgg aat gga gac ttc tta ccc acc agg ctg cag gcc cag cag gat   155
Met Arg Asn Gly Asp Phe Leu Pro Thr Arg Leu Gln Ala Gln Gln Asp
                 20                  25                  30

gct gtc aac ata gtt tgt cat tca aag acc cgc agc aac cct gag aac   203
Ala Val Asn Ile Val Cys His Ser Lys Thr Arg Ser Asn Pro Glu Asn
             35                  40                  45

aac gtg ggc ctt atc aca ctg gct aat gac tgt gaa gtg ctg acc aca   251
Asn Val Gly Leu Ile Thr Leu Ala Asn Asp Cys Glu Val Leu Thr Thr
         50                  55                  60

ctc acc cca gac act ggc cgt atc ctg tcc aag cta cat act gtc caa   299
Leu Thr Pro Asp Thr Gly Arg Ile Leu Ser Lys Leu His Thr Val Gln
     65                  70                  75

ccc aag ggc aag atc acc ttc tgc acg ggc atc cgc gtg gcc cat ctg   347
Pro Lys Gly Lys Ile Thr Phe Cys Thr Gly Ile Arg Val Ala His Leu
 80                  85                  90                  95

gct ctg aag cac cga caa ggc aag aat cac aag atg cgc atc att gcc   395
Ala Leu Lys His Arg Gln Gly Lys Asn His Lys Met Arg Ile Ile Ala
                100                 105                 110

ttt gtg gga agc cca gtg gag gac aat gag aag gat ctg gtg aaa ctg   443
Phe Val Gly Ser Pro Val Glu Asp Asn Glu Lys Asp Leu Val Lys Leu
            115                 120                 125

gct aaa cgc ctc aag aag gag aaa gta aat gtt gac att atc aat ttt   491
Ala Lys Arg Leu Lys Lys Glu Lys Val Asn Val Asp Ile Ile Asn Phe
        130                 135                 140

ggg gaa gag gag gtg aac aca gaa aag ctg aca gcc ttt gta aac acg   539
Gly Glu Glu Glu Val Asn Thr Glu Lys Leu Thr Ala Phe Val Asn Thr
    145                 150                 155

ttg aat ggc aaa gat gga acc ggt tct cat ctg gtg aca gtg cct cct   587
Leu Asn Gly Lys Asp Gly Thr Gly Ser His Leu Val Thr Val Pro Pro
160                 165                 170                 175

ggg ccc agt ttg gct gat gct ctc atc agt tct ccg att ttg gct ggt   635
Gly Pro Ser Leu Ala Asp Ala Leu Ile Ser Ser Pro Ile Leu Ala Gly
                180                 185                 190

gaa ggt ggt gcc atg ctg ggt ctt ggt gcc agt gac ttt gaa ttt gga   683
Glu Gly Gly Ala Met Leu Gly Leu Gly Ala Ser Asp Phe Glu Phe Gly
            195                 200                 205

gta gat ccc agt gct gat cct gag ctg gcc ttg gcc ctt cgt gta tct   731
Val Asp Pro Ser Ala Asp Pro Glu Leu Ala Leu Ala Leu Arg Val Ser
        210                 215                 220
```

```
atg gaa gag cag cgg cac gca gga gga gga gcg cgg cgg gca gct cga   779
Met Glu Glu Gln Arg His Ala Gly Gly Gly Ala Arg Arg Ala Ala Arg
    225                 230                 235

gct tct gct gct gag gcc ggg att gct acg act ggg act gaa gac tca   827
Ala Ser Ala Ala Glu Ala Gly Ile Ala Thr Thr Gly Thr Glu Asp Ser
240                 245                 250                 255

gac gat gcc ctg ctg aag atg acc atc agc cag caa gag ttt ggc cgc   875
Asp Asp Ala Leu Leu Lys Met Thr Ile Ser Gln Gln Glu Phe Gly Arg
                260                 265                 270

act ggg ctt cct gac cta agc agt agt act gag gaa gag gag att gct   923
Thr Gly Leu Pro Asp Leu Ser Ser Ser Thr Glu Glu Glu Glu Ile Ala
            275                 280                 285

tat gcc atg cag atg tcc ctg cag gga gca gag ttt ggc cag gcg gaa   971
Tyr Ala Met Gln Met Ser Leu Gln Gly Ala Glu Phe Gly Gln Ala Glu
        290                 295                 300

tca gca gac att gat gcc agc tca gct atg gac aca tct gag cca gcc   1019
Ser Ala Asp Ile Asp Ala Ser Ser Ala Met Asp Thr Ser Glu Pro Ala
    305                 310                 315

aag gag gag gat gat tac gac gtg atg cag gac ccc gag ttc ctt cag   1067
Lys Glu Glu Asp Asp Tyr Asp Val Met Gln Asp Pro Glu Phe Leu Gln
320                 325                 330                 335

agt gtc cta gag aac ctc cca ggt gtg gat ccc aac aat gaa gcc att   1115
Ser Val Leu Glu Asn Leu Pro Gly Val Asp Pro Asn Asn Glu Ala Ile
                340                 345                 350

cga aat gct atg ggc tcc ctg cct ccc agg cca cca agg acg gca aga   1163
Arg Asn Ala Met Gly Ser Leu Pro Pro Arg Pro Pro Arg Thr Ala Arg
            355                 360                 365

agg aca aga agg agg aag aca aga agt gag act gga ggg aaa ggg       1208
Arg Thr Arg Arg Arg Lys Thr Arg Ser Glu Thr Gly Gly Lys Gly
        370                 375                 380

tagctgagtc tgcttagggg actgggaagc acggaatata gggttagatg tggttatctg 1268

taaccattac agcctaaata aagcttggca acttttaaaa aaaaaaaaaa aaaaa      1323
```

<210> 3
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic amino acid sequence

<220>
<221> MOD_RES
<222> (1)..(35)
<223> This region may or may not be present

<220>
<221> MOD_RES
<222> (38)
<223> His, Arg or Lys

<220>
<221> MOD_RES
<222> (39)
<223> Ser or Leu

<220>
<221> MOD_RES
<222> (41)
<223> Thr or Ala

<220>
<221> MOD_RES
<222> (43)..(46)
<223> This region may or may not be present

<400> 3
Met Val Leu Glu Ser Thr Met Val Cys Val Asp Asn Ser Glu Tyr Met
1 5 10 15

Arg Asn Gly Asp Phe Leu Pro Thr Arg Leu Gln Ala Gln Gln Asp Ala
20 25 30

Val Asn Ile Val Cys Xaa Xaa Lys Xaa Arg Ser Asn Pro Glu
35 40 45

<210> 4
<211> 51
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
amino acid sequence

<220>
<221> MOD_RES
<222> (1)..(35)
<223> This region may or may not be present

<220>
<221> MOD_RES
<222> (38)
<223> His, Arg or Lys

<220>
<221> MOD_RES
<222> (39)
<223> Ser or Leu

<220>
<221> MOD_RES
<222> (41)
<223> Thr or Ala

<220>
<221> MOD_RES
<222> (43)..(51)
<223> This region may or may not be present

<400> 4
Met Val Leu Glu Ser Thr Met Val Cys Val Asp Asn Ser Glu Tyr Met
1 5 10 15

Arg Asn Gly Asp Phe Leu Pro Thr Arg Leu Gln Ala Gln Gln Asp Ala
20 25 30

Val Asn Ile Val Cys Xaa Xaa Lys Xaa Arg Ser Asn Pro Glu Asn Asn
35 40 45

Val Gly Leu
50

<210> 5
<211> 80
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic amino acid sequence

<220>
<221> MOD_RES
<222> (1)..(35)
<223> This region may or may not be present

<220>
<221> MOD_RES
<222> (38)
<223> His, Arg or Lys

<220>
<221> MOD_RES
<222> (39)
<223> Ser or Leu

<220>
<221> MOD_RES
<222> (41)
<223> Thr or Ala

<220>
<221> MOD_RES
<222> (43)..(80)
<223> This region may or may not be present

<400> 5
Met Val Leu Glu Ser Thr Met Val Cys Val Asp Asn Ser Glu Tyr Met
1 5 10 15

Arg Asn Gly Asp Phe Leu Pro Thr Arg Leu Gln Ala Gln Gln Asp Ala
20 25 30

Val Asn Ile Val Cys Xaa Xaa Lys Xaa Arg Ser Asn Pro Glu Asn Asn
35 40 45

Val Gly Leu Ile Thr Leu Ala Asn Asp Cys Glu Val Leu Thr Thr Leu
50 55 60

Thr Pro Asp Thr Gly Arg Ile Leu Ser Lys Leu His Thr Val Gln Pro
65 70 75 80

<210> 6
<211> 163
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic amino acid sequence

<220>
<221> MOD_RES
<222> (1)..(35)
<223> This region may or may not be present

<220>
<221> MOD_RES
<222> (38)
<223> His, Arg or Lys

<220>
<221> MOD_RES
<222> (39)
<223> Ser or Leu

<220>
<221> MOD_RES
<222> (41)
<223> Thr or Ala

<220>
<221> MOD_RES
<222> (43)..(163)
<223> This region may or may not be present

<400> 6

```
Met Val Leu Glu Ser Thr Met Val Cys Val Asp Asn Ser Glu Tyr Met
  1               5                  10                  15

Arg Asn Gly Asp Phe Leu Pro Thr Arg Leu Gln Ala Gln Gln Asp Ala
             20                  25                  30

Val Asn Ile Val Cys Xaa Xaa Lys Xaa Arg Ser Asn Pro Glu Asn Asn
         35                  40                  45

Val Gly Leu Ile Thr Leu Ala Asn Asp Cys Glu Val Leu Thr Thr Leu
     50                  55                  60

Thr Pro Asp Thr Gly Arg Ile Leu Ser Lys Leu His Thr Val Gln Pro
 65                  70                  75                  80

Lys Gly Lys Ile Thr Phe Cys Thr Gly Ile Arg Val Ala His Leu Ala
                 85                  90                  95

Leu Lys His Arg Gln Gly Lys Asn His Lys Met Arg Ile Ile Ala Phe
            100                 105                 110

Val Gly Ser Pro Val Glu Asp Asn Glu Lys Asp Leu Val Lys Leu Ala
        115                 120                 125

Lys Arg Leu Lys Lys Glu Lys Val Asn Val Asp Ile Ile Asn Phe Gly
    130                 135                 140

Glu Glu Glu Val Asn Thr Glu Lys Leu Thr Ala Phe Val Asn Thr Leu
145                 150                 155                 160

Asn Gly Lys
```